SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Polymeropoulus, Mihael
                 Lavedan, Christian
                 Leroy, Elisabeth
                 Nussbaum, Robert
                 Johnson, William
                 Duvoisin, Roger

    (ii) TITLE OF INVENTION: Cloning of a gene mutation for
         Parkinson's disease

    (iii) NUMBER OF SEQUENCES: 10

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: SPENCER & FRANK
        (B) STREET: 1100 New York Ave. Suite 300 East
        (C) CITY: Washington
        (D) STATE: D.C.
        (E) COUNTRY: USA
        (F) ZIP: 20005-3955

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE: 25-JUN-1998
        (C) CLASSIFICATION:

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Schneller, John W.
        (B) REGISTRATION NUMBER: 26,031
        (C) REFERENCE/DOCKET NUMBER: NIH 0082A

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (202)414-4000
        (B) TELEFAX: (202)414-4040

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 216 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
    (B) CLONE: alpha synuclein gene/ exon 4 region

(viii) POSITION IN GENOME:
    (A) CHROMOSOME/SEGMENT: 4
    (B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GCTAATCAGC AATTTAAGGC TAGCTTGAGA CTTATGTCTT GAATTTGTTT TTGTAGGCTC      60

CAAAACCAAG GAGGGAGTGG TGCATGGTGT GACAACAGGT AAGCTCCATT GTGCTTATAT     120

CAAAGATGAT ATNTAAAGTAT CTAGTGATTA GTGTGGCCCA GTATCAAGAT TCCTATGAA    181

                                                                     216
ATTGTAAAACA ATCACTGAGC ATCTAAGAAC ATATC
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "primer #3"

    (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
                                                                      22
GCTAATCAGC AATTTAGGCT AG
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "primer #13"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTATACAAGA ATCTACGAGT C   21

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 140 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: not relevant

    (ii) MOLECULE TYPE: peptide

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Homo sapiens
        (C) INDIVIDUAL ISOLATE: Swiss-Prot P37840

    (vii) IMMEDIATE SOURCE:
        (B) CLONE: alpha synuclein protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu Gly Val Val
1   5   10   15

Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Ala Glu Ala Ala Gly Lys
                20   25   30

Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val
        35   40   45

Val His Gly Val Ala Thr Val Ala Glu Lys Thr Lys Glu Gln Val Thr
        50   55   60

Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys
65   70   75   80

Thr Val Glu Gly Ala Gly Ser Ile Ala Ala Ala Thr Gly Phe Val Lys
                85   90   95

Lys Asp Gln Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln Glu Gly Ile
                100   105   110

Leu Glu Asp Met Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro

```
           115                120                   125
```

Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala
```
      130                135                   140
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 140 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: not relevant

    (ii) MOLECULE TYPE: peptide

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Rattus norvegicus
        (C) INDIVIDUAL ISOLATE: Swiss-Prot P37377

   (vii) IMMEDIATE SOURCE:
        (B) CLONE: alpha synuclein protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu Gly Val Val
```
1               5                  10                     15
```

Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Ala Glu Ala Ala Gly Lys
```
            20                25                     30
```

Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val
```
         35                40                     45
```

Val His Gly Val Thr Thr Val Ala Glu Lys Thr Lys Glu Gln Val Thr
```
      50                55                     60
```

Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys
```
65                70                     75                     80
```

Thr Val Glu Gly Ala Gly Asn Ile Ala Ala Ala Thr Gly Phe Val Lys
```
            85                90                     95
```

Lys Asp Gln Met Gly Lys Gly Glu Glu Gly Tyr Pro Gln Glu Gly Ile
```
         100               105                    110
```

Leu Glu Asp Met Pro Val Asp Pro Ser Ser Glu Ala Tyr Glu Met Pro
```
      115               120                    125
```

Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala

130   135   140

(2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 134 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: not relevant
            (D) TOPOLOGY: not relevant

        (ii) MOLECULE TYPE: peptide

        (iii) HYPOTHETICAL: NO

        (iv) ANTI-SENSE: NO

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Bos taurus
            (C) INDIVIDUAL ISOLATE: Swiss-Prot P33567

        (vii) IMMEDIATE SOURCE:
            (B) CLONE: alpha synuclein protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

        Met Asp Val Phe Met Lys Gly Leu Ser Met Ala Lys Glu Gly Val Val
        1   5   10   15

        Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Thr Glu Ala Ala Glu Lys
                    20   25   30

        Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val
                    35   40   45

        Val Gln Gly Val Ala Ser Val Ala Glu Lys Thr Lys Glu Gln Ala Ser
            50   55   60

        His Leu Gly Gly Ala Val Phe Ser Gly Ala Gly Asn Ile Ala Ala Ala
        65   70   75   80

        Thr Gly Leu Val Lys Lys Glu Glu Phe Pro Thr Asp Leu Lys Pro Glu
                        85   90   95

        Glu Val Ala Gln Glu Ala Ala Glu Glu Pro Leu Ile Glu Pro Leu Met
                    100   105   110

        Glu Pro Glu Gly Glu Ser Tyr Glu Glu Gln Pro Gln Glu Glu Tyr Gln
                    115   120   125

        Glu Tyr Glu Pro Glu Ala
            130

(2) INFORMATION FOR SEQ ID NO:7:

-51-

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 142 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: not relevant
        (D) TOPOLOGY: not relevant

   (ii) MOLECULE TYPE: peptide

  (iii) HYPOTHETICAL: NO

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Serinus canaria
        (C) INDIVIDUAL ISOLATE: genbank L33860

  (vii) IMMEDIATE SOURCE:
        (B) CLONE: alpha synuclein homologue

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

   Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu Val Val Ala
   1   5   10   15

   Ala Ala Glu Lys Thr Lys Gln Gly Val Ala Glu Ala Ala Gly Lys Thr
                   20   25   30

   Lys Glu Gly Val Leu Tyr Val Gly Ser Arg Thr Lys Glu Gly Val Val
                   35   40   45

   His Gly Val Thr Thr Val Ala Glu Lys Thr Lys Glu Gln Val Ser Asn
       50   55   60

   Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys Thr
   65   70   75   80

   Val Glu Gly Ala Gly Asn Ile Ala Ala Ala Thr Gly Leu Val Lys Lys
                       85   90   95

   Asp Gln Leu Ala Lys Gln Asn Glu Glu Gly Phe Leu Gln Glu Gly Met
                   100   105   110

   Val Asn Asn Thr Gly Ala Ala Val Asp Pro Asp Asn Glu Ala Tyr Glu
                   115   120   125

   Met Pro Pro Glu Glu Glu Tyr Gln Asp Tyr Glu Pro Glu Ala
       130   135   140

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 143 amino acids

         (B) TYPE: amino acid
         (C) STRANDEDNESS: not relevant
         (D) TOPOLOGY: not relevant

   (ii) MOLECULE TYPE: peptide

  (iii) HYPOTHETICAL: NO

   (iv) ANTI-SENSE: NO

   (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Torpedo californica
        (C) INDIVIDUAL ISOLATE: Swiss-Prot P37379

  (vii) IMMEDIATE SOURCE:
        (B) CLONE: alpha synuclein homologue

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

   Met Asp Val Leu Lys Lys Gly Phe Ser Phe Ala Lys Glu Gly Val Val
   1   5   10   15

   Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Gln Asp Ala Ala Glu Lys
                   20   25   30

   Thr Lys Gln Gly Val Gln Asp Ala Ala Glu Lys Thr Lys Glu Gly Val
            35   40   45

   Met Tyr Val Gly Thr Lys Thr Lys Glu Gly Val Val Gln Ser Val Asn
       50   55   60

   Thr Val Thr Glu Lys Thr Lys Glu Gln Ala Asn Val Val Gly Gly Ala
   65   70   75   80

   Val Val Ala Gly Val Asn Thr Val Ala Ser Lys Thr Val Glu Gly Val
                   85   90   95

   Glu Asn Val Ala Ala Ala Ser Gly Val Val Lys Leu Asp Glu His Gly
                   100   105   110

   Arg Glu Ile Pro Ala Glu Gln Val Ala Glu Gly Lys Gln Thr Thr Gln
                   115   120   125

   Glu Pro Leu Val Glu Ala Thr Glu Ala Thr Glu Glu Thr Gly Lys
                   130   135   140

(2) INFORMATION FOR SEQ ID NO:9:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 19 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "primer #1F"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

19

ACGACAGTGT GTGTAAAGG

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid
        (A) DESCRIPTION: /desc = "primer #13R"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

20

AACATCTGTC AGCAGATCTC

(2) INFORMATION FOR SEQ ID NO:11

    (i) SEQUENCE CHARACTERISITCS

        (A) LENGTH: 2809 base pairs

        (B) TYPE: NUCLEIC ACID

        (C) STRANDEDNESS: DOUBLE

        (D) TOPOLOGY: LINEAR

    (ii) MOLECULAR TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (v) IMMEDIATE SOURCE:

        (A) CLONE: BAC clone 139A20 HUMAN BETA SYNULEIN GENE

(vi)SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCGCCGCAGC CGCCGCTCCA TCCCCAGCCC CGGCCCCGCA TCCGGTTTGG AAGGGGGCTG

CAAGTTTGCA AGGGGCCCGG GANAAAAANC GAGCAGTGGC CCTTCCCGCG TCCCCAGGGT

TTCAAGGGAC GCTAGGANTN TCCGCGGCCC TGGAGGTTCG CACTGGGGAG TGGGGTGAGA

TGGGGGGAAA GCGGGAGGGG GCTCAGGGTC CAGAAGGGCN CCGCGGTCTC GGGAGTAGGG

GGGCATNTGC GTCCCGCGGG AGGGGCTGGG GTGAGAGTGC GGGGCCAGTG CACCGGTGCC

CGTGTATCGC CCTCCCCAGG CCGCCAGGAT GGACGTGTTC ATGAAGGGCC TGTCCATGGC

CAAGGAGGGC GTTGTGGCAG CCGCGGAGAA AACCAAGCAG GGGGTCACCG AGGCGGCGGA

GAAGACCAAG GAGGGCGTCC TCTACGTCGG TGGGCNGGGG GCNGGGTTTC TGGGGCTGCA

GGGCTGGGGG TCCCCCTACA GTGTGGAGCT GGGGCCGGGT CCCGGGGAGG GGGGTTCTGG

GCAAGATAAT ATNANTCAGC AGATGGGGCN AGGTCANCAN GGGTCATAAG GGACATACCC

ANCCCATAGA ANCCTGGGTC TGTATCCGGA AATGGGGACA CGGGGCGGGC TGATGAGGTG

GGGGGCTCCA NCTGAAAGGC CAGGGACCAN TGCANTNATA AAANCACACA NCCTCCTTTT

TCTTATCTTT TTTACCATTA TTAATAGTTA TCTGGTGTTG AACACTTTCT GTATGCCAAG

TACTGGGTAA AATGTCATAA CATCCATTTC CTCATGTAAT GCTTCCGCCC ATTCTACAGG

TAAGGGAAAC TGGGCTTCCC ATTGGTAGNT AAATTTTAGG TTCAGAAAGG CTTGAATTGA

ATGTCAGTTC AGCCAATTTC TTAGTGGTGG AACCAAACTG AGTTCCATCC GTGAAACGGG

GACAATAACA GCACCCGCTT CCCAGGGCTG GGGAAAAGTG AAGTGCAGCG GGGCAGGCAG

AGGACTTGAC ACAGCACTGG CCCTCAGCCA ACATCCACTA GAGGGGTGGG GTATCGCATC

AGGTGGGAGA GAACTGCAAC CCTTGCAGAC AGAGGTGTGG GGCCCAGTGC AGTGATAAGA

CGGGGGTTAA CATGGGGGTG CAGGTTGTAG GATNTGGGGA CCCAAGGAGG CAGTGACGGG

GCCAGGATGC CCACTCTGTA ATCACCATGC TGTGCTGGAG TTTCTGTTCC CTCAGCGCAG

AGTCCTTAAA TGTGCCGCTT TTTCTNCCCT GCAGGAAGCA AGACCCGAGA AGGTGTGGTA

CAAGGTGTGG CTTCAGGTAC TAGCCCAGCC CTGGCACCAG CCCTTCTCTC AMTTAGGCGG

ATGATCTGGC CGGGAACCAG AGGGCGGGGG CGGGGGAGAC TCCCAAGGCT TCTGCGGGAA

TGCTCCGTGG GGAGGGCAGG CCCTGGGATA CTACAAGGCA GGGCATCGGT GTTTCCCCCT

GGCTCCCAAA CCCCTTCCTC AACCCCCTCC CTGCTCCAGT GGCTGAAAAA ACCAAGGAAC

AGGCCTCACA TCTGGGAGGA GCTGTGTTCT CTGGGGCAGG GAACATCGCA GCAGCCACAG

GACTGGTGAA GAGGGAGGAA TTCCCTACTG ATCTGAAGGT AAGCGATCCT TCTGACCCGC

ACATGCAGGC AAACACACAC ACACACACAC ACACACACCN GGCACACAAA TAAACCTGTC

ACCATCCCCG CCCCCCTAAT CCTGCCACCA GCTTGGAACA CAAGCCACTT TGCCTCCCAT

CCTGCNGGCC CGTGCTAGAC TCAGCTCAGA ATGCATCTGA ATAANGGCGT GCATGGGTGT

GACGCTCCCG GTGATGGGGA CCCAGACCTG GCTGTCTGCG TGTATCCTGC TTGCCAGCGT

GACCCATATG ACTTCTGGCC ACGTCTGCAT GTGTCAATGA TTGTTCATTC ATTTCTTTTC

ATTCAACAAA TATCCATGCC ANANCCAGCC CTGTCCTTGA GCTTCCAGNT CCCTTTCAGC

CNAGGGGAGC NTGAGGGTTA TTTTTGGGGT CCCGATGCCC AGCACAGAGC CTGACACAAA

GGATGAGGCA TAAGCTGGTG ANTGAGTATC CAAATGGTGG AAGTGTGGAG GNTGCCAGGC

ATTGGGGGAG CGGCGTGGAG AGCCAGCTCC CCAATCCATG CTGCCACTTC AACTGTGATT

CGGGGGAATT TCCCCCTTCA CCTCCATCCC ACTTCCAAGG CACTCCAAAT AAATAACTGA

ATTAGAAATT ATCCTTGTTT TGCCAACCCA CCCTAGCCTT CCCCACTCCA ACCCACCCAA

AGCTTACCAC TGTGGGAATT TGGGGGGCAT CCTGGCTGTC CTCACGAGTC CTGACCTTTT

CTGCCCACAG CCAGAGGAAG TGGCCCAGGA AGCTGCTGAA GAACCACTGA TTGAGCCCCT

GATGGAGCCA GAAGGGGAGA GTTATGAGGA CCCACCCCAG GAGGAATATC AGGAGTATGA

GCCAGAGGCG TAGGGGCCCA GGAGAGCCCC CACCAGCAGC ACAATTCTGT CCCTGTCCCT

GCCCCGCCCC CCAGAGCCAG GGCTGTCCTT AGACTCCTTC TCCCCAATCA CGAGATCTTC

CTTCCGCTCT GAGGCAACCC CCTCGGAGCC TGTGTTAGTG TCTGTCCATC TGTCTGTCCT

ACCCGCCCGC GTCCAACCCC GGGGCATGGA CAGGGCCAGG GTTGCGGTCG CGGCTGGGAG

CCTCGCCCCT CCAGTGTTGC CTCCTCCCAT CCAGCGTCTG CGCG

(2) INFORMATION FOR SEQ ID NO:12

    (i) SEQUENCE CHARACTERISITCS

        (A) LENGTH: 223 base pairs

        (B) TYPE: NUCLEIC ACID

        (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) IMMEDIATE SOURCE:

    (A) CLONE: BAC clone 174P13 HUMAN GAMMA SYNULEIN GENE, 5' END

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGGGAGATCC AGCTCCGTCC TGCCTGCAGC AGCACAACCC TGCACACCCA CCATGGATGT

CTTCAAGAAG GGCTTCTCCA TCGCCAAGGA GGGNGTGGTG GGTGCGGTGG AAAAGACCAA

GCAGGGGGTG ACGGAAGCAG CTGAGAAGAC CAAGGAGGGG GTCATGTATG TGGGATTACA

TTTTTTTTTT AAAGAAAGAA TAAATTAATT GTGATTAAAG TTG

(2) INFORMATION FOR SEQ ID NO:13

    (i) SEQUENCE CHARACTERISITCS

        (A) LENGTH:677

        (B) TYPENUCLEIC ACID

        (C) STRANDEDNESS:DOUBLE

        (D) TOPOLOGY: LINEAR

    (ii) MOLECULAR TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (v) IMMEDIATE SOURCE:

        (A) CLONE: BAC clone 174P13 HUMAN GAMMA SYNULEIN GENE, 3' END

    (vi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTTTTTNAGG GGGGAAAACA GGGAATANAA AAANANGGGG GGGGGTTTTT NNGGGGGGGG

GGGGAAAANG GTTNGGGGGN NAACCNAAAN AAANNCCNAN GGGGGGGGNN ANTNAANTTT

TGGGAACCCA AAGCCCNAGG AGGATTTTTN GTNAANAACG TNACCTCNAG TGGGNCGAGG

AAGACCAAGG AAANGCCCAA CNCGGTTGAN CGAGGCTGTG GTGAACANCG TNCAACNCTG

TGCCCNCCAA NANCGTGGAG GNGGCGGAGA ACATCSCGGT CACCTCCGGG GTGGTGCGCM

AGGAGGACTT GAGGCCATCT KCCCCCCMAC AGGAGGGTGT GGCATCCMAA GARAAAGAGG

AAGTGGCAGA GGAGGCCCAG AGTGGGGGAR ACTAGAGGGC TACAGGCCAG CGTGGATGAC

CTGAAGAGCG CTCCTCTGCC TTGGACACCA TCCCCTCCTA GCACAAGGAG TGCCCGCCTT

GAGTGACATG CGGCTGCCCA CGCTCCTGCC CTCGTCTTCC TGGCCACCCT TGGCCTGTCC

ACCTGTGCTG CTGCACCAAC CTCACTGCCC TCCCTCGGCC CCACCCACCC TCTGGTCCTT

CTGACCCCAC TTATGCTGCT GTGAATTTTT TTTTTAAATG ATTCCAAATA AAACTTGAGC

CCACTCCAAA AAAAAAA

(2) INFORMATION FOR SEQ ID NO:14

    (i) SEQUENCE CHARACTERISITCS

        (A) LENGTH: 1181 base pairs

        (B) TYPE: NUCLEIC ACID

        (C) STRANDEDNESS: DOUBLE

        (D) TOPOLOGY: LINEAR

    (ii) MOLECULAR TYPE: DNA (genomic)

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (vii) IMMEDIATE SOURCE:

        (A) CLONE: human alpha synuclein gene/ exons 1 and 2 plus

flanking intron sequences

   (viii) POSITION IN GENOME:

        (A) CHROMOSOME/SEGMENT: 4

        (B) MAP POSITION: 4q21-q22

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AATTTCAGCG ATGCGAGGGC AAAGCGCTCT CGGCGGTGCG GTGTGAGCCA CCTCCCGGCG

CTGCCTGTCT CCTCCAGCAG CTCCCCAAGG GATAGGCTCT GCCCTTGGTG GTCGACCCTC

AGGCCCTCGN TCTCCCAGGN CGACTCTGAC GAGGGGTAGG GGGTGGTCCC CNGGAGGACC

CAGAGGAAAG GCNGGGACAA GAAGGGAGGG GAAGGGGAAA GAGGAAGAGG CATCATCCCT

AGCCCAACCG CTCCCGATCT CCACAAGAGT GCTCGTGACC CTAAACTTAA CGTGAGGCGC

AAAAGCGCCC CAACCTTTTC CCGCCTTGNN CCAGGCAGGC GGCTGGAGTT GATGGCTCAC

CCCGCGCCCC CTGCCCCATC CCCATCCGAG ATAGGGACGA GGAGCACGCT GCAGGGAAAG

CAGCGAGCGC CGGGAGAGGG GCGGGCAGAA GCGCTGACAA ATCAGCGGTG GGGGCGGAGA

GCCGAGGAGA AGGAGAAGGA GGAGGACTAG GAGGAGGAGG ACGGCGACGA CCAGAAGGGG

CCCAAGAGAG GGGGCGAGCG ACCGAGCGCC GCGACGCGAA GTGAGGTGCG TGCGGGCTCA

GCGCAGACCC CGGCCCGGCC CCTCCTGAGA GCGTCCTGGG CGCTCCCTCA CGCCTTGCCT

TCAAGCCTTC TGCCTTTCCA CCCTCGTGAG CGGAGAACTG GGAGTGGCCA TTCGACGACA

GGTTAGCGGG TTTGCCTCCC ACTCCCCCAG CCTCGCGTCG CCGGCTCACA GCGGCCTCCT

CTGGGGACAG TCCCCCCCGG GTGCCCCTCC GCCCTTCCTG TGCGCTCCTT TTCCTTCTTC

TTTCCTATTA AATATTATTT GGGAATTGTT TAAATTTTTT TTTTAAAAAA AGAGAGAGGC

GNGGAGGAGT CGGAGTTGTG GAGAAGCAGA GGGACTCAGG TAAGTACCTG TGGATCTAAA

CGGGNGTCTT TTGGAAATCC TGGAGAACGC CGGATGGAGA CGAATGGTCG TGGGNACCGG

GAGGGGGTGG TGCTGCCATG AGGACCGCTG GGCCAGGTCT CTGGGAGGTG AGTACTTGTC

CTTTGGGGAG CTAAGGAAAG AGACTTGACC TGGCTTTCGT CCTGCTTCTG ATATTCCCTT

CTCCACAAGG GCTGAGAGNT TAGGCTGCTT CTCCGGGATC C

(2) INFORMATION FOR SEQ ID NO:15

    (i) SEQUENCE CHARACTERISITCS

        (A) LENGTH: 536 base pairs

        (B) TYPE: NUCLEIC ACID

        (C) STRANDEDNESS: DOUBLE

        (D) TOPOLOGY: LINEAR

(ii)MOLECULAR TYPE: DNA (genomic)

(iii)HYPOTHETICAL: NO

(iv)ANTI-SENSE: NO

(vii)IMMEDIATE SOURCE:

(A)CLONE: human alpha synuclein gene/ exon 3 plus flanking

intron sequences

(viii)POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTTAAAAGAG TCTCACACTT TGGAGGGTTT CTCATGATTT TTCAGTGTTT TTTGTTTATT

TTTCCCCGAA AGTTCTCATT CAAAGTGTAT TTTATGTTTT CCAGTGTGGT GTAAAGAAAT

TCATTAGCCA TGGATGTATT CATGAAAGGA CTTTCAAAGG CCAAGGAGGG AGTTGTGGCT

GCTGCTGAGA AAACCAAACA GGGTGTGGCA GAAGCAGCAG GAAAGACAAA AGAGGGTGTT

CTCTATGTAG GTAGGTAAAC CCCAAATGTC AGTTTGGTGC TTGTTCATGA GTGATGGGTT

AGGATAACAA TACTCTAAAT GCTGGTAGTT CTCTCTCTTG ATTCATTTTT GCATCATTGC

TTGTCAAAAA GGTGGACTGA GTCAGAGGTA TGTGTAGGTA GGTGAATGTG AACGTGTGTA

TNTGAGCTAA TAGTAAAAAT GCGACTGTTT GCTTTTCAGA TTTTTAATTT TGCCTAATAT

NTATGACTTN TTAAAATGAA TGTTTCTGTA CTACATAATT CTATNTCAGA GACAGT

(2) INFORMATION FOR SEQ ID NO:16

(i)SEQUENCE CHARACTERISITCS

(A)LENGTH: 650 base pairs

(B)TYPE: NUCLEIC ACID

(C)STRANDEDNESS:DOUBLE

(D)TOPOLOGY: LINEAR

(ii)MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(A) CLONE: human alpha synuclein gene/ exon 4 plus flanking
intron sequences

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGCAGGTCA ACGGATCTGT CTCTAGTGCT GTACTTTTAA AGCTTCTACA GTTCTGAATT

CAAAATTATC TTCTCACTGG GCCCCGGTGT TATCTCATTC TTTTTTCTCC TCTGTAAGTT

GACATGTGAT GTGGGAACAA AGGGGATAAA GTCATTATTT TGTGCTAAAA TCGTAATTGG

AGAGGACCTC CTGTTAGCTG GGCTTTCTTC TATNTATTGT GGTGGTTAGG AGTTCCTTCT

TCTAGTTTTA GGATATATAT ATATATTTTT TCTTTCCCTG AAGATATAAT AATATATATA

CTTCTGAAGA TTGAGATTTT TAAATTAGTT GTATTGAAAA CTAGCTAATC AGCAATTTAA

GGCTAGCTTG AGACTTATGT CTTGAATTTG TTTTTGTAGG CTCCAAAACC AAGGAGGGAG

TGGTGCATGG TGTGGCAACA GGTAAGCTCC ATTGTGCTTA TATCAAAGAT GATATNTAAA

GTATCTAGTG ATTAGTGTGG CCCAGTATCA AGATTCCTAT TGAAATTGTA AAACAATCAC

TGAGCATCTA AGAACATATC AGTCTTATTG AAACTGAATT CTTTATAAAG TATTTTTAAA

TAGGTAAATA TTGATTATAA ATAAAAAATA TACTTGCCAA GAATAATGAG

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISITCS

(A) LENGTH: 504 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii)MOLECULAR TYPE: DNA (genomic)

(iii)HYPOTHETICAL: NO

(iv)ANTI-SENSE: NO

(vii)IMMEDIATE SOURCE:

(A)CLONE: human alpha synuclein gene/ exon 5 plus flanking

intron sequences

(viii)POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATATCTTAGC CAAGATTCAA TGTTTGGTTG AACCACACTC ACTTGACATC TTGGTGGCTT

TTGTTTCTTC TGACCACTCA GTTATCTATG GCATGTGTAG ATACAGGTGT ATGGAANCGA

TGGCTAGTGG AAGTGGAATG ATTTTAAGTC ACTGTTATTC TACCACCCTT TAATCTGTTG

TTGCTCTTTA TTTGTACCAG TGGCTGAGAA GACCAAAGAG CAAGTGACAA ATGTTGGAGG

AGCAGTGGTG ACGGGTGTGA CAGCAGTAGC CCAGAAGACA GTGGAGGGAG CAGGGAGCAT

TGCAGCAGCC ACTGGCTTTG TCAAAAAGGA CCAGTTGGGC AAGGTATGGC TGTGTACGTT

TTGTGTTACA TTTATAAGCT GGTGAGATTA CGGTTCATTT TCATGTGAAG CCTGGAGGCA

GGAGCAAGAT ACTTACTGTG GGGAACGGCT ACCTGACCCT CCCCTTGTGA AAAAGTGCTA

CCTTTATATT GGTCTTGCTT GTTT

(2) INFORMATION FOR SEQ ID NO:18

(i)SEQUENCE CHARACTERISITCS

(A)LENGTH: 727 base pairs

(B)TYPE: NUCLEIC ACID

(C)STRANDEDNESS:DOUBLE

(D)TOPOLOGY: LINEAR

(ii)MOLECULAR TYPE: DNA (genomic)

(iii)HYPOTHETICAL: NO

(iv)ANTI-SENSE: NO

(vii)IMMEDIATE SOURCE:

(A)CLONE: human alpha synuclein gene/ exons 1 and 2 plus flanking intron sequences

(viii)POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AAAAGTTTAC ATACTTTGAG GTTGATAACC CATGTTGCCG CAATGTTTCC CCGGAGGCAT

TGTGGAGTTT AGAATGCCAG TAGTAATATT AAGGTGTGCC ATTTTCAAGA TCCGTGGCCA

ACATCCCTAT ATGTAAGATT TTTCCAAAAC ATGGTTCTGA TTTTTAAAAG TGAAAAATGC

TACTTCATCA TGTTCTTTTT GTGCTTCTTA CTTTAAATAT TAGAATGAAG AAGGAGCCCC

ACAGGAAGGA ATTCTGGAAG ATATGCCTGT GGATCCTGAC AATGAGGCTT ATGAAATGCC

TTCTGAGGTA GGAGTCCAAG CTGAATCTTT CTAACAAGAC AGTACCAAAA ACCTGTCATT

GTCACATTTC TCTTTCATTA GTGCTTAGTG AGAATCATTT GCTCTCTACA TGCTCATTA

GTGGACAACT TGCAAGTTAA GAATAGTTTT TACATTTTTA AAGGGTCCTT AAAAAAAAAG

AGGAGGAGGA AGATGAAGAA GAGGAAGAAA GGATGTAAAA GAAATCATAT GTAGTCCACA

TAGCTTAATA TACNTACTAC TTGACCCTTT ACAGGAAAAG CTTTACTAAC CCCTGCATTA

GAGAATATAT TTTTTTGCAA AAACATTGAT TGTAAATTTT AGTGTAAAGT GGGGAGCCAT

TTCCTATCTC ATTGGCTGTC CAGTGCTGAT GCGTAATTGA AACTTATACT AACAGTGTGT

GCTGTCT

(2) INFORMATION FOR SEQ ID NO:19

(i)SEQUENCE CHARACTERISITCS

(A)LENGTH: 1596 base pairs

(B)TYPE: NUCLEIC ACID

(C) STRANDEDNESS:DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(A) CLONE: human alpha synuclein gene/ exon 7 plus flanking intron sequences

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 4

(B) MAP POSITION: 4q21-q22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTTTGATTTT TCTAATATTA GGAAGGGTAT CAAGACTACG AACCTGAAGC CTAAGAAATA

TCTTTGCTCC CAGTTTCTTG AGATCTGCTG ACAGATGTTC CATCCTGTAC AAGTGCTCAG

TTCCAATGTG CCCAGTCATG ACATTTCTCA AAGTTTTTAC AGTGTATCTC GAAGTCTTCC

ATCAGCAGTG ATTGAAGCAT CTGTACCTGC CCCCACTCAG CATTTCGGTG CTTCCCTTTC

ACTGAAGTGA ATACATGGTA GCAGGGTCTT TGTGTGCTGT GGATTTTGTG GCTTCAATCT

ACGATGTTAA AACAAATTAA AAACACCTAA GTGACTACCA CTTATTTCTA AATCCTCACT

ATTTTTTTGT TGCTGTTGTT CAGAAGTTGT TAGTGATTTG CTATCATATA TTATNAGATT

TTTAGGTGTC TTTTAATGAT ACTGTCTAAG AATAATGACG TATTGTGAAA TTTGTTAATA

TATATNATAC TTAAAAATAT GTGAGCATGA AACTATGCAC CTATAATACT AAATATGAAA

TTTTACCATT TTGCGATGTG TTTTATTCAC TTGTGTTTGT ATATNAATGG TGAGAATTAA

AATAAAACGT TATCTCATTG CAAAAATATT TTATTTTTAT CCCATCTCAC TTTAATAATA

AAAATCATGC TTATAAGCAA CATGAATTAA GAACTGACAC AAAGGACAAA AATATAAAGT

TATTAATAGC CATTTGAAGA AGGAGGAATT TTAGAAGAGG TAGAGAAAAT GGAACATTAA

CCCTACACTC GGAATTCCCT GAAGCAACAC TGCCAGAAGT GTGTTTTGGT ATGCACTGGT

TCCTTAAGTG GCTGTGATTA ATTATTGAAA GTGGGGTGTT GAAGACCCCA ACTACTATTG

TAGAGTGGTC TATTTCTCCC TTCAATCCTG TCAATGTTTG CTTTACGTAT TTTGGGGAAC

TGTTGTTTGA TGTGTATGTG TTTATAATTG TTATACATTT TTAATTGAGC CTTTTATTAA

CATATATTGT TATTTTTGTC TCGAAATAAT TTTTTAGTTA AAATCTATTT TGTCTGATAT

TGGTGTGAAT GCTGTACCTT TCTGACAATA AATAATATNC GACCATGAAT AAAAAAAAAA

AAAAAGTGGG TTCCCGGGAA CTAAGCAGTG TAGAAGATGA TTTTGACTAC ACCCTCCTTA

GAGAGCCATA AGACACATTA GCACATATTA GCACATTCAA GGCTCTGAGA GAATGTGGTT

AACTTTGTTT AACTCAGCAT TCCTCACTTT TTTTTTTTAA TCATCAGAAA TTCTCTCTCT

CTCTCTCTTT TTCTCTCGCT CTCTTTTTTT TTTTTTTTTT TTTTACAGGA AATGCCTTTA

AACATCGTTG GGAACTACCA GAGTCACCTT AAAGGGAGNA TCAATTCTCT AGGACTGGAT

AAAAATTTCA TGGGCCTCCT TTAAAATGTT GCCCAAATAT ATGGAATTCT AGGGGTTTTT

CCNTAGGGGG AAGGGTTTTT TCTCTTTTCN GGGGAGGATC CTTTTAACNC CCCNGGGGGG

NGCCCGGAAA ATAAACTTGG NGGGGGGGNA AAACTT